IT IS CLAIMED:

1. An isolated polypeptide comprising (A) a first amino acid sequence at the amino terminus of said polypeptide wherein said first amino acid sequence corresponds to an amino acid sequence of the carboxy terminus of a chemokine, and (B) a second amino acid sequence corresponding to the amino acid sequence of a hapten.

2. The isolated polypeptide of claim 1, wherein said chemokine is human chemokine and said hapten is an amino acid sequence corresponding to the Meningitis Related Homologous Antigenic Sequences (MRHAS).

3. The isolated polypeptide of claim 2, having the amino acid sequence is KEAVVFVTKLKREVCADPKKEWVQTYIKNLDR-QQQPPKA.

4. A vaccine for preventing disease in a mammalian host comprising (A) a polypeptide according to claim 1, and (B) a pharmaceutically or veterinarilly acceptable carrier, diluent or excipient.

5. The vaccine according to claim 4, wherein said chemokine is a human chemokine and said hapten is an amino acid sequence corresponding to the MRHAS.

6. The vaccine according to claim 5, wherein said polypeptide has the amino acid sequence KEAVVFVTKLKREVCADPKKEWVQTYIKNLDR-QQQPPKA.

7. A method of preventing infection of a human by a meningitis-causing organism comprising administering to said human an amount of a vaccine according to claim 5 which is sufficient to elicit a protective immune response.

8. A method of preventing infection of a human by a meningitis-causing organism comprising administering to said human an amount of a vaccine according to claim 6 which is sufficient to elicit a protective immune response.

9. A composition comprising an antibody that binds polypeptide containing a MRHAS.

10. A process for raising antibodies to meningitis etiologic agents which comprises administering to a host a protective amount of a peptide having the formula:

a---X---b

wherein:

X is a sequence of at least 7 amino acids taken as a block selected from the group comprising:

(i) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{102}--AA_{108} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(ii) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{89}--AA_{95} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(iii) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{313}--AA_{319} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(iv) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{103}--AA_{109} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(v) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{90}--AA_{96} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(vi) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{314}--AA_{320} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(vii) the amino acid sequence of the Gag Polyprotein of an isolate of the HIV-1 that corresponds to AA_{145}--AA_{151} of the Gag Polyprotein of the LV isolate of HIV-1 as set forth in FIGURE 3;

(viii) the amino acid sequence of the Envelope Polyprotein Precursor of an isolate of the HIV-1 that corresponds to AA_{655} to AA_{661} of the Envelope Polyprotein Precursor of the LAV-1a isolate of HIV-1 as set forth in FIGURE 4;

(ix) the amino acid sequence that corresponds to AA_{99}--AA_{105} of the Lipoprotein E Precursor of *Haemophilus influenzae* as set forth in FIGURE 5;

(x) the amino acid sequence that corresponds to AA_1 to AA_5 of the Opacity-Related Protein POPM3 of *Neisseria meningitidis* as set forth in FIGURE 6;

(xi) the amino acid sequence that corresponds to AA_{423} to AA_{429} of the Pneumococcal Surface Protein A of *Streptococcus pneumoniae* as set forth in FIGURE 7;

(xii) the amino acid sequence that corresponds to AA_{151}--AA_{157} of the Protein P60 Precursor of Listeria *monocytogenes* as set forth in FIGURE 8;

(xiii) the amino acid sequence that corresponds to AA_{181}--AA_{187} of the Protein P60 Precursor of Listeria *monocytogenes* as set forth in FIGURE 8;

(xiv) from the amino acid sequence of that corresponds to AA_{249}--AA_{255} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xv) from the amino acid sequence that corresponds to AA_{292}--AA_{298} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xvi) from the amino acid sequence of a variant of the chemokine human Monocyte Chemoattractant Factor hMCP-1, that corresponds to AA_{93}--AA_{99} of hMCP-1 as set forth in FIGURE 9;

(xvii) from the amino acid sequence of the chemokine hMCP-3, that corresponds to AA_{61}--AA_{67} of hMCP-3 as set forth in FIGURE 10; and

(xviii) from any amino acid sequence present within a protein that is homologous to members of the MRHAS family;

with said block maintaining the sequence in the N terminus to C terminus direction of the native amino acid sequence and analogue thereof, said analogues resulting from conservative substitutions in or modifications to the native amino acid sequence block;

a is selected from the group consisting of:
(i) an amino terminus;
(ii) one to eight amino acids taken as a block from and maintaining the sequence and N terminus to C terminus direction of that portion of the native amino acid sequence of the protein immediately N-terminal to said X or conservative substitutions in or modifications thereto; and

(iii) a substituent effective to facilitate coupling of the peptide to another moiety; and

b is selected from the group consisting of:

(i) a carboxy terminus;
(ii) one to eight amino acids taken as a block from and maintaining the sequence and N terminus to C terminus direction of that portion of the native amino acid sequence of the protein immediately C-terminal to said X or conservative substitutions in or modifications thereto; and
(iii) a substituent effective to facilitate coupling of the peptide to another moiety.

11. A meningitis vaccine comprising a protective amount of a peptide having the formula:

a---X---b

wherein:

X is a sequence of at least 7 amino acids taken as a block selected from the group comprising:

(i) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{102}--AA_{108} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(ii) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{89}--AA_{95} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(iii) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{313}--AA_{319} of said protein of the M33 strain of Rubella virus as set forth in FIGURE 1;

(iv) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{103}--AA_{109} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(v) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{90}--AA_{96} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(vi) the amino acid sequence of the Structural Polyprotein of a strain of Rubella virus that corresponds to AA_{314}--AA_{320} of said protein of the Therien strain of Rubella virus as set forth in FIGURE 2;

(vii) the amino acid sequence of the Gag Polyprotein of an isolate of the HIV-1 that corresponds to AA_{145}--AA_{151} of the Gag Polyprotein of the LV isolate of HIV-1 as set forth in FIGURE 3;

(viii) the amino acid sequence of the Envelope Polyprotein Precursor of an isolate of the HIV-1 that corresponds to AA_{655} to AA_{661} of the Envelope Polyprotein Precursor of the LAV-1a isolate of HIV-1 as set forth in FIGURE 4;

(ix) the amino acid sequence that corresponds to AA_{99}--AA_{105} of the Lipoprotein E Precursor of *Haemophilus influenzae* as set forth in FIGURE 5;

(x) the amino acid sequence that corresponds to AA_1 to AA_5 of the Opacity-Related Protein POPM3 of *Neisseria meningitidis* as set forth in FIGURE 6;

(xi) the amino acid sequence that corresponds to AA_{423} to AA_{429} of the Pneumococcal Surface Protein A of *Streptococcus pneumoniae* as set forth in FIGURE 7;

(xii) the amino acid sequence that corresponds to AA_{151}--AA_{157} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xiii) the amino acid sequence that corresponds to AA_{181}--AA_{187} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xiv) from the amino acid sequence of that corresponds to AA_{249}--AA_{255} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xv) from the amino acid sequence that corresponds to AA_{292}--AA_{298} of the Protein P60 Precursor of *Listeria monocytogenes* as set forth in FIGURE 8;

(xvi) from the amino acid sequence of a variant of the chemokine human Monocyte Chemoattractant Factor hMCP-1, that corresponds to AA_{93}--AA_{99} of hMCP-1 as set forth in FIGURE 9;

(xvii) from the amino acid sequence of the chemokine hMCP-3, that corresponds to AA_{61}--AA_{67} of hMCP-3 as set forth in FIGURE 10; and

(xviii) from any amino acid sequence present within a protein that is homologous to members of the MRHAS family;

with said block maintaining the sequence in the N terminus to C terminus direction of the native amino acid sequence and analogue thereof, said analogues resulting from conservative substitutions in or modifications to the native amino acid sequence block;

a is selected from the group consisting of:

(i) an amino terminus;

(ii) one to eight amino acids taken as a block from and maintaining the sequence and N terminus to C

terminus direction of that portion of the native amino acid sequence of the protein immediately N-terminal to said X or conservative substitutions in or modifications thereto; and

(iii) a substituent effective to facilitate coupling of the peptide to another moiety; and

b is selected from the group consisting of:

(i) a carboxy terminus;

(ii) one to eight amino acids taken as a block from and maintaining the sequence and N terminus to C terminus direction of that portion of the native amino acid sequence of the protein immediately C-terminal to said X or conservative substitutions in or modifications thereto; and

(iii) a substituent effective to facilitate coupling of the peptide to another moiety.

12. A method for protecting a human against disease caused by bacterial and/or viral meningitis etiologic agents comprising administering an effective dose of the vaccine according to claim 5.

13. A method for protecting a human against disease caused by bacterial and/or viral meningitis etiologic agents comprising administering an effective dose of the composition according to claim 10.